

of each amino acid residue contained in the amino acid sequence of each reference protein whose three-dimensional structure is predetermined, and wherein said method comprises: conducting matching based on the environmental information of each amino acid residue of each reference protein and hydrophobicity or hydrophilicity property of the side chain of each amino acid residue of the query sequence, choosing at least one protein as a template protein from the reference proteins that has high similarity in three-dimensional structure to the protein comprising the query sequence, and predicting the scaffold of the protein comprising a query sequence.

2. (Amended) The method according to claim 1, wherein the amino acid sequence of each of the reference proteins is divided into two or more segment sequences comprising two or more continuous amino acid residues based on the characteristics of the three-dimensional structure of the reference protein.

3. (Amended) The method according to claim 2, wherein the amino acid sequence of each of the reference proteins is divided into one or more core segment sequences which are predetermined to form a hydrophobic core, and into one or more sub segment sequences which are not predetermined to form a hydrophobic core.

4. (Twice-Amended) The method according to claim 1, wherein the matching is conducted based on the information on degree of burial into the inside of the protein of the side chain of each amino acid residue in the reference protein, or degree of exposure to the protein surface of the side chain of each amino acid residue in the reference protein, together with the properties of hydrophobicity or hydrophilicity of each amino acid residue in the query sequence.

B3 7. (Twice-Amended) The method according to claim 1, wherein the matching comprises: matching by sliding one or more core segment sequences on the query sequence, optionally considering gaps at one end or both ends of the core segment sequences, provided when two or more core segment sequences are used, the core segment sequences are placed in the order of appearance on the amino acid sequence of the reference protein; and, sliding one or more sub segment sequences on the query sequence, optionally considering one or more gaps.

B4 11. (Twice-Amended) A database in a computer readable medium which contains environmental information on the side chains of amino acid residues of one or more reference proteins with predetermined three-dimensional structures, and which is used for the method according to claim 1.

Please add new claims 12- 20

12. A database in a computer readable medium which contains environmental information on the side chains of amino acid residues of one or more reference proteins with predetermined three-dimensional structures, and which is used for the method according to claim 2.

B4 13. A database in a computer readable medium which contains environmental information on the side chains of amino acid residues of one or more reference proteins with predetermined three-dimensional structures, and which is used for the method according to claim 3.

14. A database in a computer readable medium which contains environmental information on the side chains of amino acid residues of one or more reference proteins with predetermined three-dimensional structures, and which is used for the method according to claim 4.

15. A database in a computer readable medium which contains environmental information on the side chains of amino acid residues of one or more reference proteins with predetermined three-dimensional structures, and which is used for the method according to claim 5.

16. A database in a computer readable medium which contains environmental information on the side chains of amino acid residues of one or more reference proteins with predetermined three-dimensional structures, and which is used for the method according to claim 6.

B4 17. A database in a computer readable medium which contains environmental information on the side chains of amino acid residues of one or more reference proteins with predetermined three-dimensional structures, and which is used for the method according to claim 7.

18 A database in a computer readable medium which contains environmental information on the side chains of amino acid residues of one or more reference proteins with predetermined three-dimensional structures, and which is used for the method according to claim 8.

19 A database in a computer readable medium which contains environmental information on the side chains of amino acid residues of one or more reference proteins with predetermined three-dimensional structures, and which is used for the method according to claim 9.

20. A database in a computer readable medium which contains environmental information on the side chains of amino acid residues of one or more reference proteins with predetermined three-dimensional structures, and which is used for the method according to claim 10.